

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 18, 2001, 14:28:24 ; Search time 13.85 Seconds
(without alignments)
1135.814 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004

Sequence: 1 MTSPPSSSPVRLFTLDGGE.....EDEDGASENVVPVQLQSN 764

Scoring table:

BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1645.5	41.1	839	US-09-197-636-2	Sequence 2, Appl1
2	1644.5	41.1	839	US-09-197-636-8	Sequence 8, Appl1
3	1638.5	40.9	839	US-09-197-636-4	Sequence 4, Appl1
4	151	3.8	1839	US-09-172-977-4	Sequence 4, Appl1
5	150	3.7	1088	US-09-082-059-2	Sequence 2, Appl1
6	148	3.7	843	US-09-172-977-3	Sequence 3, Appl1
7	146	3.6	1095	US-09-112-096-15	Sequence 15, Appl1
8	138.5	3.5	352	US-09-065-474-139	Sequence 139, Appl1
9	138.5	3.5	1745	US-09-031-485-33	Sequence 33, Appl1
10	138.5	3.5	1745	US-08-847-429A-33	Sequence 33, Appl1
11	138.5	3.5	1745	US-09-065-474-33	Sequence 33, Appl1
12	137	3.4	1533	US-08-623-679-9	Sequence 9, Appl1
13	137	3.4	1533	US-08-933-774-9	Sequence 9, Appl1
14	137	3.4	1533	US-09-181-030-9	Sequence 9, Appl1
15	131	3.3	303	US-09-031-485-23	Sequence 23, Appl1
16	131	3.3	303	US-08-847-429A-23	Sequence 23, Appl1
17	131	3.3	303	US-09-065-474-23	Sequence 23, Appl1
18	129	3.2	348	US-09-031-485-28	Sequence 28, Appl1
19	129	3.2	348	US-08-847-429A-28	Sequence 28, Appl1
20	129	3.2	348	US-09-065-474-28	Sequence 28, Appl1
21	127	3.2	300	US-08-897-340-32	Sequence 32, Appl1
22	127	3.2	300	US-09-252-329-32	Sequence 32, Appl1
23	126	3.1	551	US-08-699-103B-25	Sequence 25, Appl1
24	125.5	3.1	787	US-09-188-930-334	Sequence 334, Appl1
25	125.5	3.1	1139	US-08-537-210A-4	Sequence 4, Appl1
26	125.5	3.1	1139	US-09-113-825-4	Sequence 4, Appl1
27	125.5	3.1	2703	US-08-185-432-19	Sequence 19, Appl1

28	123.5	3.1	191	US-09-031-485-20	Sequence 20, Appl1
29	123.5	3.1	191	US-08-847-429A-20	Sequence 20, Appl1
30	123.5	3.1	191	US-09-065-474-20	Sequence 20, Appl1
31	122	3.0	741	US-08-943-956A-2	Sequence 2, Appl1
32	120.5	3.0	302	US-09-031-485-38	Sequence 38, Appl1
33	120.5	3.0	302	US-08-847-429A-38	Sequence 38, Appl1
34	120.5	3.0	302	US-09-065-474-38	Sequence 38, Appl1
35	120.5	3.0	741	US-08-462-481-2	Sequence 2, Appl1
36	120.5	3.0	741	US-08-436-771-2	Sequence 2, Appl1
37	120.5	3.0	741	US-08-436-771-4	Sequence 4, Appl1
38	120.5	3.0	741	US-08-434-998-2	Sequence 4, Appl1
39	120.5	3.0	741	US-08-434-998-4	Sequence 4, Appl1
40	120.5	3.0	741	US-08-487-797-2	Sequence 2, Appl1
41	120.5	3.0	741	US-08-487-797-4	Sequence 4, Appl1
42	120.5	3.0	741	US-08-701-005A-2	Sequence 2, Appl1
43	120.5	3.0	741	US-08-479-895-2	Sequence 2, Appl1
44	120.5	3.0	741	PCT-US95-02058-2	Sequence 2, Appl1
45	120.5	3.0	741	PCT-US95-02058-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DICKMORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P. O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,636
; FILING DATE: 23-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9805137.8
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: UK 9815791.0
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: UK 9819278.4
; FILING DATE: 03-SEP-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 839 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-197-636-2

Query Match	41.1%;	Score 1645.5;	DB 4;	Length 839;
Best Local Similarity	48.5%;	Pred. No. 9.5e-147;		
Matches 344;	Conservative 121;	Mismatches 200;	Indels 45;	Gaps 11;

QY	74	FDRORLENNASRGVPEBLLAGLPELSTSKYLLDSETBESTGKTCMLKAVYLLKQGVNA	133
Db	113	YDRSRIFEVAQAONNCODLESLLLEFLQSKKHLLDNEKDEPDEKTCITLKMILLHBOQNT	172
QY	134	CITLPLQIDRDSGNRPOELVNAOCTDDVYRCHSAHLAIKERSLQCYKLLIENGANYNHAR	193
Db	173	TIPLLLEIARQDTSCLKELVNASYDSYKKGOTALLHIAIEBRNNALVTLLEVNGADYQAAA	232
QY	194	CGRFQKGGOG--TCYFEBELPLSLAACRKMDDVSYLLENHQASLQADTDSQNTVYLAH	252
Db	233	HGDFEFKTKGPGPYFEGELPLSLACRNOGLGYKFLLONSWQDPAISAROSVNTVYLAH	292
QY	253	VMSIDNSAENIALTYSYDGLQAGARLCPYVQLEDIRNLQDTPILPLAKAEKGIETFRH	312
Db	293	VEVADNTADNKTFTYSMYNEILLIGAKLHPTLKEELTNKKGMTPALAAGTGKIGVLA	352
QY	313	ILQREFS--GLSHSRKFTKCYCPVAVSYLDASVDSCENSYLELIAF--HCKSPRRHR	369
Db	353	ILQREIDIEPCCRHLRSKRFTEAAGVSHSSYLDSCIDTCEKNSYLEVIAVSSETPRHRD	412
QY	370	MVYLEPINKLLQAKMDLLIP--PEFLNLCMLIYEIFTAAYAHQPTLKROAAPHKAE-V	427
Db	413	MLVLEPILNRLLQDKMDRFKVRKIEFNFNLVCLVMIIFTMAAYRPV---DGLRPFKMEKT	469
QY	428	GNSMLLTGCHILLIGIYLLVGLQMLVRRHVFITWISFIDSYELLPLFQALLTVVSQVL	487
Db	470	GDEVRYVGEILSYLVGGVYFFERQIOYFLQRRSPSKLTFVDSYSEMLFLOSLTLMATVYL	529
QY	488	CEFLAIEMVLLFSLVAVLGNLLYLYRGRONHGISVMOXLYLRLFEILLIYVFLF	547
Db	530	YFSHLKEVNASMVSIALGWTNMLYTRGRQOQMCIVAMIEKMLIRDLCPFMFVYIVFLF	589
QY	548	GFAVALVSLSQEA-----WRPEAPGPNATESVQPMQEGDEGNGAQRGIL	594
Db	590	GFSTAAVYLLIEDGKNDLSLPSESTSHMRRCACRPDDSS-----YNSLY	632
QY	595	EASLELRFETIGMKELARFOEDLHGRGVULLLLAVYLLTYTILLNMILAMSEFVSVAAT	654
Db	633	STCLELRFETIGMDLETEYDRKAAFTILLLAIVYLLTYTILLNMILAMGEFVANKIAO	692
QY	655	DSMSIWLKOKAISYLEMENGYMWC--RKKORAGVALLVTRKPDGSPDERMCFRYEEVMMAS	713
Db	693	ESKNIMWKQRAITILIDPEKSPFLKMRKAPFSGKILQYGYTPDGKDDVDMCFRDEVENMTT	752
QY	714	WEQILPLTLCEDPSGA--GVPTLLENPVYLASPKKEDDGCASENTYVPVQOLQ	762
Db	753	WNTVANGIINEDPGNCEGVYKRLTSLFSSK---RVSGSRHMKNNALVPLLR	798

RESULT 2
 US-09-197-636-8
 Sequence 8, Application US/09197636
 Patent No. 6239267
 GENERAL INFORMATION:
 APPLICANT: DICKMORTH, DAVID
 APPLICANT: HAYES, PHILIP
 APPLICANT: MEADOWS, HELEN
 APPLICANT: DAVIDS, JOHN
 TITLE OF INVENTION: NOVEL COMPOUNDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rainer & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: US
 ZIP: 19482-0980

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-197-636-8

Query Match	41.1%	Score 1644.5	DB 4	Length 839
Best Local Similarity	48.5%	Pred. No. 1.2e-166		
Matches 344	Conservative 121	Mismatches 200	Indels 45	Gaps 11
QY	74	FDRLDLPFNAVARGVPEDLAGLPREYLSKTSKYLTJDSYEATGSGKTCMLKAVLNLGDGYNA	133	
		: : : : : : : : : : : : : : :		
Db	113	YDRSIFFAVAVQNNQODLESLLFLQKSKHNLTDHFNDPEFGKCLLKAMLNHDCGNT	172	
QY	134	CILPLLDIDRDSGNPQPLVNAQCTDDYVIRGSHALHIAIEKSLQCVKLLVENGAVHARA	193	
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Db	173	TIPLLLEIAROTDSLKELEYNAASYDSSYKGGOTALHIAIEERRMMAVLTVLVENGADVOAAA	232	
QY	194	CGRFQKQCG--TCFFEGELPLSLAACTQWQVSVLLDENPQAPALQATDSQGNVTLAL	252	
		: : : : : : : : : : : : : :		
Db	233	HGDFEKKRKGPRGFEGLPLSLAACTQWQVSVLLDENPQAPALQATDSQGNVTLAL	292	
QY	253	VMISDMSAENIALVTSWVDGLQAGARICPTQVOLDIRNLQDLPFLPLAKAREGKTEIFRH	312	
		: : : : : : : : : : : : : :		
Db	293	VEVADNTADNRKFTYSWNEILLIGAKLHPPLKLEBELLNKKGMPTLALAGAGKIGVLAY	352	
QY	313	ILQREFS--GLSHLSRKFTWCYGPVRVSLYVDLASVDSCEENSVLEIIAF--HCKSPARRH	369	
		: : : : : : : : : : : : : :		
Db	353	ILQREIQPECRHLSRKFTEMAGVSHSVLSDICIDCEKNSVLEVIAYSSSETPNRHD	412	
QY	370	MVYLEPLKLQAKWDLIRP--FLINFLCNILYMTFLFAVAHYOHTLKKQAAPHKAE--V	427	
		: : : : : : : : : : : : : :		
Db	413	MLVEPLRLRLQDKDRDVRKRIFFENFLVYLCYLIIFFMAIYPRV---DGLPRKMKET	469	
QY	428	GNSMLLTGHIILILGGIYLLVGLQWLYEMRRHVFIMISFDSFELFLFOALLPVSQVL	487	
		: : : : : : : : : : : : : :		
Db	470	GDYFRVTEILLSTVAGVYFFFRGLOYFLQRRPSMKTLLEVDSYSEMLFLQSLFMALATVVL	529	
QY	488	CFLAIEWPLVSLVSLVGLNLTLYTTRGFOHTGIYSVMIOKVLIRDLIRFLLIYVLEFL	547	
		: : : : : : : : : : : : : :		
Db	530	YFSHKKEVAVASWFSIALGWTNMLYTRGPFQGMGIYAMIEKMILRLDLCRFMYVYVLEFL	589	
QY	548	GFAVALVSLSDFA-----WRPEAPCTGNATESVQPMEGQDEGNGAOYRGL	594	
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Db	590	GFSTAVVLLIDGKNDLSLPSESTSHRMGSPACRPDSS-----YNSLYL	632	

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0y 74 FDRDRLEFNAVSRGVEDLAGIPEYLLSTSKYLTDESYEAGSTGKTCIMKAVLNLDGVNA 133
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Db 113 YDRSIFEAVAQNQCDELLESLTLFLQSKKHXYDNFNDPETGKTCCLKKMLNLHDGQNT 172

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Query Match	3.8%;	Score 151;	DB 2;	Length 1839;
Best Local Similarity	27.3%;	Pred. No. 7.1e-05;		
Matches	88;	Conservative	46;	Mismatches 96;
			Indels	92;
			Gaps	19;

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